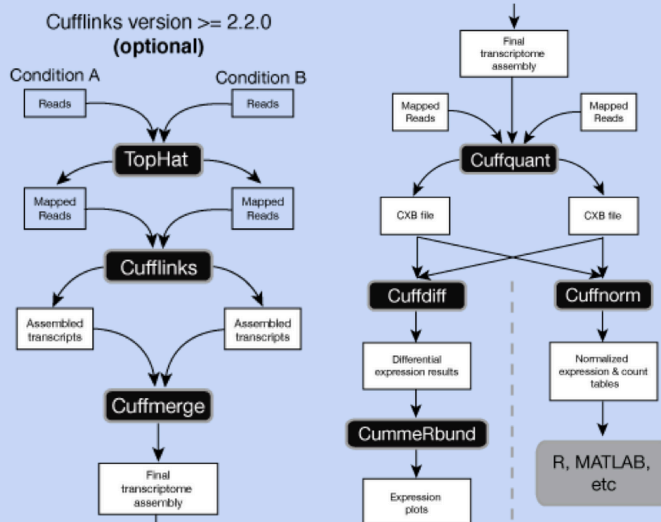# Bioinformatics Pipeline

Tuxedo Suite

ccb.jhu.edu/software/tophat/manual.shtml

Steps Required:

- Align reads
- Assemble transcripts
- Quantify transcripts
- Compare across samples
- Visualize
- Downstream analysis